

SEQUENCE LISTING

<110> Scott, Fred W.

<120> Recombinant Multivalent Viral Vaccine

<130> 18617.0016

<140> 08/552,369

<141> November 3, 1995

<160> 25

<210> 1

<211> 2254

<212> DNA

<213> feline panieukopenia virus

<220>

<223>

<400> 1

atg agt gat gga gca gtt caa cca gac ggt ggt caa cct gct gtc	45
Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val	
5 10 15	

aga aat gaa aga gct aca gga tct ggg aac ggg tct gga ggc ggg	90
Arg Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly	
20 25 30	

ggt ggt ggt ggt tct ggg ggt gtg ggg att tct acg ggt act ttc	135
Gly Gly Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe	
35 40 45	

aat aat cag acg gaa ttt aaa ttt ttg gaa aac gga tgg gtg gaa	180
Asn Asn Gln Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu	
50 55 60	

atc aca gca aac tca agc aga ctt gta cat tta aat atg cca gaa	225
---	-----

Ile Thr Ala Asn Ser Ser Arg Leu Val His Leu Asn Met Pro Glu
65 70 75

agt gaa aat tat aaa aga gta gtt gta aat aat atg gat aaa act 270
Ser Glu Asn Tyr Lys Arg Val Val Val Asn Asn Met Asp Lys Thr
80 85 90

gca gtt aaa gga aac atg gct tta gat gac act cat gta caa att 315
Ala Val Lys Gly Asn Met Ala Leu Asp Asp Thr His Val Gln Ile
95 100 105

gta aca cct tgg tca ttg gtt gat gca aat gct tgg gga gtt tgg 360
Val Thr Pro Trp Ser Leu Val Asp Ala Asn Ala Trp Gly Val Trp
110 115 120

ttt aat cca gga gat tgg caa cta att gtt aat act atg agt gag 405
Phe Asn Pro Gly Asp Trp Gln Leu Ile Val Asn Thr Met Ser Glu
125 130 135

ttg cat tta gtt agt ttt gaa caa gaa att ttt aat gtt gtt tta 450
Leu His Leu Val Ser Phe Glu Gln Glu Ile Phe Asn Val Val Leu
140 145 150

aag act gtt tca gaa tct gct act cag cca cca act aaa gtt tat 495
Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro Thr Lys Val Tyr
155 160 165

aat aat gat tta act gca tca ttg atg gtt gca tta gat agt aat 540
Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu Asp Ser Asn
170 175 180

aat act atg cca ttt act cca gca gct atg aga tct gag aca ttg 585
Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu Thr Leu
185 190 195

ggt ttt tat cca tgg aaa cca acc ata cca act cca tgg aga tat 630
Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg Tyr
200 205 210

tat ttt caa tgg gat aga aca tta ata cca tct cat act gga act 675
Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr
215 220 225

agt ggc aca cca aca aat ata tat cat ggt aca gat cca gat gat	720
Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp	
230 235 240	
gtt caa ttt tat act att gaa aat tct gtg cca gta cac tta cta	765
Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu	
245 250 255	
aga aca ggt gat gaa ttt gct aca gga aca ttt ttt ttt gat tgt	810
Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys	
260 265 270	
aaa cca tgt aga cta aca cat aca tgg caa aca aac aga gca ttg	855
Lys Pro Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu	
275 280 285	
ggc tta cca cca ttt cta aat tct ttg cct caa tct gaa gga gct	900
Gly Leu Pro Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala	
290 295 300	
act aac ttt ggt gat ata gga gtt caa caa gat aaa aga cgt ggt	945
Thr Asn Phe Gly Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly	
305 310 315	
gta act caa atg gga aat aca gac tat att act gaa gct act att	990
Val Thr Gln Met Gly Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile	
320 325 330	
atg aga cca gct gag gtt ggt tat agt gca cca tat tat tct ttt	1035
Met Arg Pro Ala Glu Val Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe	
335 340 345	
gaa gcg tct aca caa ggg cca ttt aaa ata cct att gca gca gga	1080
Glu Ala Ser Thr Gln Gly Pro Phe Lys Ile Pro Ile Ala Ala Gly	
350 355 360	
cgg ggg gga gcg caa aca gat gaa aat caa gca gca gat ggt gat	1125
Arg Gly Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala Asp Gly Asp	
365 370 375	
cca aga tat gca ttt ggt aga caa cat ggt caa aaa act act aca	1170
Pro Arg Tyr Ala Phe Gly Arg Gln His Gly Gln Lys Thr Thr Thr	
380 385 390	
aca gga gaa aca cct gag aga ttt aca tat ata gca cat caa gat	1215

09373891.060401

Thr Gly Glu Thr	Pro Glu Arg Phe Thr Tyr Ile Ala His Gln Asp	
	395	400 405
aca gga aga tat	cca gca gga gat tgg att caa aat att aac ttt	1260
Thr Gly Arg Tyr	Pro Ala Gly Asp Trp Ile Gln Asn Ile Asn Phe	
	410	415 420
aac ctt cct gta	aca aat gat aat gta ttg cta cca aca gat cca	1305
Asn Leu Pro Val	Thr Asn Asp Asn Val Leu Leu Pro Thr Asp Pro	
	425	430 435
att gga ggt aaa	aca gga atc aac tat act aat ata ttt aat act	1350
Ile Gly Gly Lys	Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn Thr	
	440	445 450
tat ggt cct tta	act gca tta aat aat gta cca cca gtt tat cca	1395
Tyr Gly Pro Leu	Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro	
	455	460 465
aat ggt caa att	tgg gat aaa gaa ttt gat act gac tta aaa cca	1440
Asn Gly Gln Ile	Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro	
	470	475 480
aga ctt cat gta	aat gca cca ttt gtt tgt caa aat aat tgt cct	1485
Arg Leu His Val	Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro	
	485	490 495
ggt caa tta ttt	gta aaa gtt gcg cct aat tta aca aat gaa tat	1530
Gly Gln Leu Phe	Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr	
	500	505 510
gat cct gat gca	tct gct aat atg tca aga att gta act tac tca	1575
Asp Pro Asp Ala	Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser	
	515	520 525
gat ttt tgg tgg	aaa ggt aaa tta gta ttt aaa gct aaa cta aga	1620
Asp Phe Trp Trp	Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg	
	530	535 540
gca tct cat act	tgg aat cca att caa caa atg agt att aat gta	1665
Ala Ser His Thr	Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val	
	545	550 555
gat aac caa ttt	aac tat cta cca aat aat att gga gct atg aaa	1710

Asp Asn Gln Phe Asn Tyr Leu Pro Asn Asn Ile Gly Ala Met Lys	
560	565 570
att gta tat gaa aaa tct caa cta gca cct aga aaa tta tat	1752
Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro Arg Lys Leu Tyr	
575	580
taatatactt actatgtttt tatgggttatt acatatcaac tagcacctag	1802
aaaattatat taatatactt actatgtttt tatgttttatt acatattatt	1852
ttaagattaa ttaaattaca acatagaaat attgtacttg tatttgatat	1902
aggatttaga aggtttgtta tatgggtatac aataactgta agaaatagaa	1952
gaacatttag atcatgggta gtatgggtata caataactgt aagaaataga	2002
agaacattta gatcatgggt agtagtttgt tttataaaat gtaattgtaa	2052
actattaatg tatgttggtta tgggtgtgggt ggttggttgg tttgccctta	2102
gaatatgtta aggaccaaaa aaatcaataa aagacattta aaacttaatg	2152
gtctcgtata ctgtctataa ggtgaactaa ccttaccata agtatcaact	2202
tgtctttaag ggggggggtgg gtgggagatg cacaatatca gtagactgac	2252
tg	2254

<210> 2

<211> 1575

<212> DNA

<213> rabies virus

<220>

<223>

<400>

atg gtt cct cag gct ctc ctg ttt gta ccc ctt ctg gtt ttt	42
---	----

05073391.0504401

Met	Val	Pro	Gln	Ala	Leu	Leu	Phe	Val	Pro	Leu	Leu	Val	Phe	
1				5					10					
cca	ttg	tgt	ttt	ggg	aaa	ttc	cct	att	tac	acg	ata	cta	gac	84
Pro	Leu	Cys	Phe	Gly	Lys	Phe	Pro	Ile	Tyr	Thr	Ile	Leu	Asp	
15					20					25				
aag	ctt	ggg	ccc	tgg	agc	ccg	att	gac	ata	cat	cac	ctc	agc	126
Lys	Leu	Gly	Pro	Trp	Ser	Pro	Ile	Asp	Ile	His	His	Leu	Ser	
	30					35					40			
tgc	cca	aac	aat	ttg	gta	gtg	gag	gac	gaa	gga	tgc	acc	aac	168
Cys	Pro	Asn	Asn	Leu	Val	Val	Glu	Asp	Glu	Gly	Cys	Thr	Asn	
		45					50					55		
ctg	tca	ggg	ttc	tcc	tac	atg	gaa	ctt	aaa	gtt	gga	tac	atc	210
Leu	Ser	Gly	Phe	Ser	Tyr	Met	Glu	Leu	Lys	Val	Gly	Tyr	Ile	
			60					65					70	
tta	gcc	ata	aaa	atg	aac	ggg	ttc	act	tgc	aca	ggc	gtt	gtg	252
Leu	Ala	Ile	Lys	Met	Asn	Gly	Phe	Thr	Cys	Thr	Gly	Val	Val	
				75					80					
acg	gag	gct	gaa	acc	tac	act	aac	ttc	gtt	ggg	tat	gtc	aca	294
Thr	Glu	Ala	Glu	Thr	Tyr	Thr	Asn	Phe	Val	Gly	Tyr	Val	Thr	
85					90					95				
acc	acg	ttc	aaa	aga	aag	cat	ttc	cgc	cca	aca	cca	gat	gca	336
Thr	Thr	Phe	Lys	Arg	Lys	His	Phe	Arg	Pro	Thr	Pro	Asp	Ala	
	100					105					110			
tgt	aga	gcc	gcg	tac	aac	tgg	aag	atg	gcc	ggg	gac	ccc	aga	378
Cys	Arg	Ala	Ala	Tyr	Asn	Trp	Lys	Met	Ala	Gly	Asp	Pro	Arg	
		115					120					125		
tat	gaa	gag	tct	cta	cac	aat	ccg	tac	cct	gac	tac	cgc	tgg	420
Tyr	Glu	Glu	Ser	Leu	His	Asn	Pro	Tyr	Pro	Asp	Tyr	Arg	Trp	
			130					135					140	
ctt	cga	act	gta	aaa	acc	acc	aag	gag	tct	ctc	gtt	atc	ata	462
Leu	Arg	Thr	Val	Lys	Thr	Thr	Lys	Glu	Ser	Leu	Val	Ile	Ile	
				145					150					
tct	cca	agt	gta	gca	gat	ttg	gac	cca	tat	gac	aga	tcc	ctt	504
Ser	Pro	Ser	Val	Ala	Asp	Leu	Asp	Pro	Tyr	Asp	Arg	Ser	Leu	

155											160					165					
cac	tcg	agg	gtc	ttc	cct	agc	ggg	aag	tgc	tca	gga	gta	gcg		546						
His	Ser	Arg	Val	Phe	Pro	Ser	Gly	Lys	Cys	Ser	Gly	Val	Ala								
	170					175					180										
gtg	tct	tct	acc	tac	tgc	tcc	act	aac	cac	gat	tac	acc	att		588						
Val	Ser	Ser	Thr	Tyr	Cys	Ser	Thr	Asn	His	Asp	Tyr	Thr	Ile								
		185					190					195									
tgg	atg	ccc	gag	aat	ccg	aga	cta	ggg	atg	tct	tgt	gac	att		630						
Trp	Met	Pro	Glu	Asn	Pro	Arg	Leu	Gly	Met	Ser	Cys	Asp	Ile								
			200					205					210								
ttt	acc	aat	agt	aga	ggg	aag	aga	gca	tcc	aaa	ggg	agt	gag		672						
Phe	Thr	Asn	Ser	Arg	Gly	Lys	Arg	Ala	Ser	Lys	Gly	Ser	Glu								
				215					220												
act	tgc	ggc	ttt	gta	gat	gaa	aga	ggc	cta	tat	aag	tct	tta		714						
Thr	Cys	Gly	Phe	Val	Asp	Glu	Arg	Gly	Leu	Tyr	Lys	Ser	Leu								
225					230					235											
aaa	gga	gca	tgc	aaa	ctc	aag	tta	tgt	gga	gtt	cta	gga	ctt		756						
Lys	Gly	Ala	Cys	Lys	Leu	Lys	Leu	Cys	Gly	Val	Leu	Gly	Leu								
	240					245					250										
aga	ctt	atg	gat	gga	aca	tgg	gtc	gcg	atg	caa	aca	tca	aat		798						
Arg	Leu	Met	Asp	Gly	Thr	Trp	Val	Ala	Met	Gln	Thr	Ser	Asn								
		255					260					265									
gaa	acc	aaa	tgg	tgc	gct	ccc	gat	cag	ttg	gtg	aac	ctg	cac		840						
Glu	Thr	Lys	Trp	Cys	Pro	Pro	Asp	Gln	Leu	Val	Asn	Leu	His								
			270					275					280								
gac	ttt	cgc	tca	gac	gaa	att	gag	cac	ctt	gtt	gta	gag	gag		882						
Asp	Phe	Arg	Ser	Asp	Glu	Ile	Glu	His	Leu	Val	Val	Glu	Glu								
				285					290												
ttg	gtc	agg	aag	aga	gag	gag	tgt	ctg	gat	gca	cta	gag	tcc		924						
Leu	Val	Arg	Lsy	Arg	Glu	Glu	Cys	Leu	Asp	Ala	Leu	Glu	Ser								
295					300					305											
atc	atg	aca	aac	aag	tca	gtg	agt	ttc	aga	cgt	ctc	agt	cat		966						
Ile	Met	Thr	Thr	Lys	Ser	Val	Ser	Phe	Arg	Arg	Leu	Ser	His								
	310					315					320										

tta aga aaa ctt gtc cct ggg ttt gga aaa gca tat acc ata	1008
Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile	
325 330 335	
ttc aac aag acc ttg atg gaa gcc gat gct cac tac aag tca	1050
Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser	
340 345 350	
gtc aga act tgg aat gag atc ctc cct tca aaa ggg tgt tta	1092
Val Arg Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu	
355 360	
aga gtt ggg ggg agg tgt cat cct cat gtg aac ggg gtg ttt	1134
Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe	
365 370 375	
ttc aat ggt ata ata tta gga cct gac ggc aat gtc tta atc	1176
Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile	
380 385 390	
cca gag atg caa tca tcc ctc ctc cag caa cat atg gag ttg	1218
Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu	
395 400 405	
ttg gaa tcc tcg gtt atc ccc ctt gtg cac ccc ctg gca gac	1260
Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp	
410 415 420	
ccg tct acc gtt ttc aag gac ggt gac gag gct gag gat ttt	1302
Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe	
425 430	
gtt gaa gtt cac ctt ccc gat gtg cac aat cag gtc tca gga	1344
Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly	
435 440 445	
gtt gac ttg ggt ctc ccg aac tgg ggg aag tat gta tta ctg	1386
Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu	
450 455 460	
agt gca ggg gcc ctg act gcc ttg atg ttg ata att ttc ctg	1428
Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu	
465 470 475	

atg	aca	tgt	tgt	aga	aga	gtc	aat	cga	tca	gaa	cct	acg	caa	1470
Met	Thr	Cys	Cys	Arg	Arg	Val	Asn	Arg	Ser	Glu	Pro	Thr	Gln	
		480						485					490	
cac	aat	ctc	aga	ggg	aca	ggg	agg	gag	gtg	tca	gtc	act	ccc	1512
His	Asn	Leu	Arg	Gly	Thr	Gly	Arg	Glu	Val	Ser	Val	Thr	Pro	
			495					500						
caa	agc	ggg	aag	atc	ata	tct	tca	tgg	gaa	tca	cac	aag	agt	1554
Gln	Ser	Gly	Lys	Ile	Ile	Ser	Ser	Trp	Glu	Ser	His	Lys	Ser	
505					510					515				
ggg	ggt	gag	acc	aga	ctg	tga								1575
Gly	Gly	Glu	Thr	Arg	Leu									
	520				524									

<210> 3

<211> 44

<212> DNA

<213> P11 late promoter and leader sequence

<220>

<223>

<400>
taaaaatata gtagaatttc attttgtttt tttctatgct

<210> 4

<211> 28

<212> DNA

<213> artificial sequence

<220>

<223> forward primer

<400>

cgggatccat ttttccttcg tttgccat 28

<210> 5

<211> 28

<212> DNA

<213> artificial sequence

<220> reverse primer

<223>

<400>

cgggtaccga tttctccgtg ataggtat 28

<210> 6

<211> 18

<212> DNA

<213> artificial sequence

<220> sequencing primer

<223>

<400>

ctacttgcat agataggt 18

<210> 7

<211> 2007

<212> DNA

<213> feline calicivirus

<220>

<223>

<400> 1

atg tgc tca acc tgc gct aac gtg ctt aaa tac tat gat tgg gat	45
Met Cys Ser Thr Cys Ala Asn Val Leu Lys Tyr Tyr Asp Trp Asp	
1 5 10 15	
cct cac atc aaa ttg gta atc aac ccc aac aaa ttt cta cat gtt	90
Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val	
20 25 30	
ggc ttc tgc gat aac cct tta atg tgt tgt tat cct gaa tta cta	135
Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu	
35 40 45	
cct gaa ttt ggc acc atg tgg gat tgt gat caa tcg cca ctc caa	180
Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln	
50 55 60	
gtc tac ctt gag tca atc ctg ggt gat gat gaa tgg tcc tcc act	225
Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr	
65 70 75	
cat gaa gca att gac cca gtt gtg cca cca atg cat tgg gat gaa	270
His Glu Ala Ile Asp Pro Val Val Pro Pro Met His Trp Asp Glu	
80 85 90	
gcc gga aaa atc ttc caa cca cac cct ggc gtc ctt atg cat cac	315
Ala Gly Lys Ile Phe Gln Pro His Pro Gly Val Leu Met His His	
95 100 105	
ctc atc tgt aag gtt gca gaa gga tgg gac cca aac ctg cca ctt	360
Leu Ile Cys Lys Val Ala Glu Gly Trp Asp Pro Asn Leu Pro Leu	
110 115 120	
ttc cgc ttg gaa gcg gac gat ggt tcc atc acg aca cct gaa cag	405
Phe Arg Leu Glu Ala Asp Asp Gly Ser Ile Thr Thr Pro Glu Gln	
125 130 135	
gga aca atg gtt ggt gga gtc att gct gag ccc aac gcc caa atg	450
Gly Thr Met Val Gly Gly Val Ile Ala Glu Pro Asn Ala Gln Met	
140 145 150	
tca acc gca gct gac atg gcc act ggg aaa agt gtg gac tct gag	495
Ser Thr Ala Ala Asp Met Ala Thr Gly Lys Ser Val Asp Ser Glu	

	155	160	165	
tgg gaa gcc ttc ttc tcc ttt cac act	agt gtg aac tgg agc aca	540		
Trp Glu Ala Phe Phe Ser Phe His Thr	Ser Val Asn Trp Ser Thr			
170	175	180		
tct gaa act cag ggg aag ata ctc ttt	aaa caa tcc tta gga cca	585		
Ser Glu Thr Gln Gly Lys Ile Leu Phe	Lys Gln Ser Leu Gly Pro			
185	190	195		
ttg ctc aac ccc tac ctt acc cat ctt	gca aag ctg tat gtt gct	630		
Leu Leu Asn Pro Tyr Leu Thr His Leu	Ala Lys Leu Tyr Val Ala			
200	205	210		
tgg tct ggt tct gtt gat gtt agg ttt	tct att tct gga tct ggt	675		
Trp Ser Gly Ser Val Asp Val Arg Phe	Ser Ile Ser Gly Ser Gly			
215	220	225		
gtc ttt gga ggg aaa tta gct gct att	gtt gtg ccg cca gga att	720		
Val Phe Gly Gly Lys Leu Ala Ala Ile	Val Val Pro Pro Gly Ile			
230	235	240		
gat cct gtt caa agt act tca atg ctg	caa tat cct cat gtc ctc	765		
Asp Pro Val Gln Ser Thr Ser Met Leu	Gln Tyr Pro His Val Leu			
245	250	255		
ttt gat gct cgt caa gtt gaa cct gtt	atc ttt tcc att ccc gat	810		
Phe Asp Ala Arg Gln Val Glu Pro Val	Ile Phe Ser Ile Pro Asp			
260	265	270		
cta aga agc acc tta tat cac ctt atg	tct gac act gat acc aca	855		
Leu Arg Ser Thr Leu Tyr His Leu Met	Ser Asp Thr Asp Thr Thr			
275	280	285		
tcg ttg gta atc atg gtg tac aat gat	ctt att aac ccc tat gct	900		
Ser Leu Val Ile Met Val Tyr Asn Asp	Leu Ile Asn Pro Tyr Ala			
290	295	300		
aat gac tca aac tct tcg ggc tgc att	gtc act gtg gaa act aaa	945		
Asn Asp Ser Asn Ser Ser Gly Cys Ile	Val Thr Val Glu Thr Lys			
305	310	315		
ccg ggg cca gat ttc aag ttt cac ctc	tta aaa cct cct ggg tct	990		
Pro Gly Pro Asp Phe Lys Phe His Leu	Leu Lys Pro Pro Gly Ser			
320	325	330		

atg tta act cac gga tct atc cca tct gat cta atc cca aaa tca	1035
Met Leu Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Ser	
335 340 345	
tct tcg ctt tgg att gga aat cgg ttt tgg tct gac ata acc gat	1080
Ser Ser Leu Trp Ile Gly Asn Arg Phe Trp Ser Asp Ile Thr Asp	
350 355 360	
ttt gta att cgg cct ttt gtg ttc cag gca aat cga cac ttt gat	1125
Phe Val Ile Arg Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp	
365 370 375	
ttc aac caa gag aca gca ggt tgg agc acc cca agg ttt cgc cca	1170
Phe Asn Gln Glu Thr Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro	
380 385 390	
att act atc act atc agt gtt aag gag tca gca aag ctt ggt att	1215
Ile Thr Ile Thr Ile Ser Val Lys Glu Ser Ala Lys Leu Gly Ile	
395 400 405	
gga gtg gcc acc gac tac att gtt ccc ggc ata cca gat gga tgg	1260
Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile Pro Asp Gly Trp	
410 415 420	
ccc gac aca aca atc cca ggt gag ttg gta cct gtt ggt gac tat	1305
Pro Asp Thr Thr Ile Pro Gly Glu Leu Val Pro Val Gly Asp Tyr	
425 430 435	
gcc atc act aat ggc acc aac aat gat atc acc aca gct gcg cag	1350
Ala Ile Thr Asn Gly Thr Asn Asn Asp Ile Thr Thr Ala Ala Gln	
440 445 450	
tac gat gca gcc act gag att aga aac aac acc aat ttc aga ggc	1395
Tyr Asp Ala Ala Thr Glu Ile Arg Asn Asn Thr Asn Phe Arg Gly	
455 460 465	
atg tac att tgt ggt tct ctt caa aga gct tgg ggg gat aag aag	1440
Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys	
470 475 480	
att tca aat act gct ttt atc aca acc ggc acg gtt gat gga gcc	1485
Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala	
485 490 495	

aaa ttg ata ccc agt aat acc att gac caa aca aaa att gcc gta	1530
Lys Leu Ile Pro Ser Asn Thr Ile Asp Gln Thr Lys Ile Ala Val	
500 505 510	
ttc caa gac aca cat gcg aat aag cat gtc cag acc tcg gac gac	1575
Phe Gln Asp Thr His Ala Asn Lys His Val Gln Thr Ser Asp Asp	
515 520 525	
aca ttg gcc ctg ctt ggt tat act ggt att ggt gag gaa gca att	1620
Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Glu Ala Ile	
530 535 540	
ggg gct gac cgc gat aga gtt gtg cga att agc gtc ctc ccg gaa	1665
Gly Ala Asp Arg Asp Arg Val Val Arg Ile Ser Val Leu Pro Glu	
545 550 555	
cgt ggc gca cgt ggt ggc aat cac cca atc ttc cac aaa aac tct	1710
Arg Gly Ala Arg Gly Gly Asn His Pro Ile Phe His Lys Asn Ser	
560 565 570	
atc aag ctt ggt tat gta att agg tcc att gat gtg ttc aat tct	1755
Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser	
575 580 585	
caa att ctg cat acc tct agg caa ctt tcc ctc aat cat tac tta	1800
Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu	
590 595 600	
ttg tcg cct gac tcc ttt gct gtc tat agg att att gac tct aat	1845
Leu Ser Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn	
605 610 615	
gga tcc tgg ttt gac ata ggc att gat aat gat gga ttt tct ttt	1890
Gly Ser Trp Phe Asp Ile Gly Ile Asp Asn Asp Gly Phe Ser Phe	
620 625 630	
gtt ggt gta tca agt att ggt aaa tta gag ttt cct tta act gcc	1935
Val Gly Val Ser Ser Ile Gly Lys Leu Glu Phe Pro Leu Thr Ala	
635 640 645	
tcc tac atg gga att caa ttg gca aaa att cga ctt gcc tct aac	1980
Ser Tyr Met Gly Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn	
650 655 660	
att agg agt gtg atg aca aaa tta tga	2007

Ile Arg Ser Val Met Thr Lys Leu
665

<210> 8

<211> 582

<212> DNA

<213> artificial sequence

<220> hemagglutinin left arm

<223>

<400> 1
 attaaacgca aatatccatg gaaaacgcgc agtatacaga cgattttttta 50
 cagtattttgg agagtttttat aggaagtata tagagtagaa ccagaatttt 100
 gtaaaaataa atcacatttt tataactaata tgaaacaact atcgatagtt 150
 atattgctac tatcgatagt atatacaacc aaacctcatc ctacacagat 200
 atcaaaaaaa ctaggcgatg atgctactct atcgtgtaat agaaacaata 250
 cacatggata tcttgatcag agttcttggg ataagaaacc agactccatt 300
 attctcttag cagccaaaaa cgatgtcgta tactttgatg attatacagc 350
 ggataaagta tcatacgatt caccgatga tactctagct acaattatta 400
 caattaaatc attgacatct gcagatgcag gtacttatat atgcgcattc 450
 ttataacat caacaaatga tacggataaa atagattatg aagaatactt 500
 catagatttg gttgtaaadc cagctaattgt atccactatt gacgcgattc 550
 tatcaggatc taatttctcc gtgataggta tc 582

<210> 9

<211> 447

<212> DNA

<213> artificial sequence

<220> hemagglutinin right arm

<223>

<400> 1
 ctctagcgcc taaccccagc cgaccgacga caacctttat gatacatata 50
 atgaaccaat atctgtatca tctcgtatc caacaacggt agaaagtgtt 100
 acaatatcta ctacaaaata tacaactagt gactttatag agatatttgg 150

cattgtttca	ctaattttat	tattggccgt	ggcgattttc	tgtattatat	200
tatttctgta	gtggacggtc	tcgtaaacaa	gaaacaaata	tattatagat	250
tttaactcag	ataaatgtct	ggaataatta	aatctatcgt	tttgagcgga	300
ccatctgggt	ccggcaagac	agctatagtc	aggagactct	tacaagatta	350
tggaaatata	tttggatttg	tggtatccca	taccactaga	tttcctcgtc	400
ctatggaacg	agaaggtgtc	gactaccatt	acgttaacag	agaggcc	447

<210> 10

<211> 40

<212> DNA

<213> artificial sequence

<220> primer P3

<223>

<400> 1

gatacctatc acggagaaat tagatcctga tagaatcgcg 40

<210> 11

<211> 22

<212> DNA

<213> artificial sequence

<220> primer P1

<223>

<400> 1

attaaacgca aatatccatg gg 22

<210> 12

<211> 27

<212> DNA

<213> artificial sequence

<220> primer F2

<223>

<400> 1

gcggtaccct ggggttaggc gatagag 27

<210> 13

<211> 20

<212> DNA

<213> artificial sequence

<220> primer P5

<223>

<400> 1

atttctccgt gataggtatc 20

<210> 14

<211> 22

<212> DNA

<213> artificial sequence

<220> primer P5

<223>

<400> 1

ggcctctctg ttaacgtaat gg 22

<210> 15

<211> 22

<212> DNA

<213> artificial sequence

<220> primer P2

<223>

<400> 1

gcgtcgaagt ttgagcatgt gc 22

<210> 16

<211> 40

<212> DNA

<213> artificial sequence

<220> primer P4

<223>

<400> 1

ctctagcgcc taaccccagg cgaccgacga caacctttat 40

<210> 17

<211> 840

<212> DNA

<213> feline infectious peritonitis virus

<220>

<223>

<400> 1

aaaccaaggc atataatccc gacgaagcat ttttggtttg aactaaacaa a 51

atg aag tac att ttg cta ata ctc gcg tgc ata att gca tgc gtt 96

Met	Lys	Tyr	Ile	Leu	Leu	Ile	Leu	Ala	Cys	Ile	Ile	Ala	Cys	Val	
1				5					10					15	
tat	ggg	gaa	cgc	tac	tgt	gcc	atg	caa	gac	agt	ggc	ttg	cag	tgt	141
Tyr	Gly	Glu	Arg	Tyr	Cys	Ala	Met	Gln	Asp	Ser	Gly	Leu	Gln	Cys	
				20					25					30	
att	aat	ggc	aca	aat	tca	aga	tgt	caa	acc	tgc	ttt	gaa	cgt	ggg	186
Ile	Gln	Gly	Thr	Gln	Ser	Arg	Cys	Gln	Thr	Cys	Phe	Glu	Arg	Gly	
				35					40					45	
gat	ctt	att	tgg	cat	ctt	gct	aac	tgg	aac	ttc	agc	tgg	tct	gta	231
Asp	Leu	Ile	Trp	His	Leu	Ala	Asn	Trp	Asn	Phe	Ser	Trp	Ser	Val	
				50					55					60	
ata	ttg	att	gtt	ttt	ata	aca	gtg	tta	caa	tat	ggc	aga	cca	caa	276
Ile	Leu	Ile	Val	Phe	Ile	Thr	Val	Leu	Gln	Tyr	Gly	Arg	Pro	Gln	
				65					70					75	
ttt	agc	tgg	ctc	gtt	tat	ggc	att	aaa	atg	ctg	atc	atg	tgg	cta	321
Phe	Ser	Trp	Leu	Val	Tyr	Gly	Ile	Lys	Met	Leu	Ile	Met	Trp	Leu	
				80					85					90	
tta	tgg	cct	att	gtt	cta	gcg	ctt	acg	att	ttt	aat	gca	tac	tct	366
Leu	Trp	Pro	Ile	Val	Leu	Ala	Leu	Thr	Ile	Phe	Asn	Ala	Tyr	Ser	
				95					100					105	
gag	tac	caa	gtt	tcc	aga	tat	gta	atg	ttc	ggc	ttt	agt	gtt	gca	411
Glu	Tyr	Gln	Val	Ser	Arg	Tyr	Val	Met	Phe	Gly	Phe	Ser	Val	Ala	
				110					115					120	
ggg	gca	gtt	gta	acg	ttt	gca	ctt	tgg	atg	atg	tat	ttt	gtg	aga	456
Gly	Ala	Val	Val	Thr	Phe	Ala	Leu	Trp	Met	Met	Tyr	Phe	Val	Arg	
				125						130				135	
tct	gtt	cag	cta	tat	aga	aga	acc	aaa	tca	tgg	tgg	tct	ttt	aat	501
Ser	Val	Gln	Leu	Tyr	Arg	Axg	Thr	Lys	Ser	Trp	Trp	Ser	Phe	Asn	
				140					145					150	
cct	gag	act	aat	gca	att	ctt	tgt	gtt	aat	gca	ttg	ggg	aga	agt	546
Pro	Glu	Thr	Asn	Ala	Ile	Leu	Cys	Val	Asn	Ala	Leu	Gly	Arg	Ser	
				155					160					165	
tat	gtg	ctt	ccc	tta	gat	ggg	act	cct	aca	ggg	gtt	acc	ctt	act	591
Tyr	Val	Leu	Pro	Leu	Asp	Gly	Thr	Pro	Thr	Gly	Val	Thr	Leu	Thr	

093331.030401

	170	175	180	
cta ctt tca gga aat cta tat gct gaa ggt ttc aaa atg gct ggt				636
Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys Met Ala Gly				
	185	190	195	
ggt tta acc atc gag cat ttg cct aaa tac gtc atg att gct aca				681
Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met Ile Ala Thr				
	200	205	210	
cct agt aga acc atc gtt tat aca tta gtt gga aaa caa tta aaa				726
Pro Ser Arg Thr Ile Val Tyr Thr Ile Val Gly Lys Gln Leu Lys				
	215	220	225	
gca act act gcc aca gga tgg gct tac tac gta aaa tct aaa gct				771
Ala Thr Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala				
	230	235	240	
ggt gat tac tca aca gaa gca cgt act gac aat ttg agt gaa cat				816
Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His				
	245	250	255	
gaa aaa tta tta cat atg gtg taa				840
Glu Lys Leu Leu His Met Val				
	260			
<210>	18			
<211>	1144			
<212>	DNA			
<213>	feline infectious peritonitis virus			
<220>				
<223>				
<400>	1			
atg gcc aca cag gga caa cgc gtc aac tgg gga gat gaa cct tcc				45
Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser				
1 5 10 15				
aaa aga cgt ggt cgt tct aac tct cgt ggt cgg aag aat aat gat				90
Lys Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp				

20										25					30					
ata	cct	ttg	tca	ttc	tac	aac	ccc	att	acc	ctc	gaa	caa	gga	tct	135					
Ile	Pro	Leu	Ser	Phe	Tyr	Asn	Phe	Ile	Thr	Leu	Glu	Gln	Glu	Ser						
				35					40					45						
aaa	ttt	tgg	aat	tta	tgt	ccg	aga	gac	ctt	gtt	ccc	aaa	gga	ata	180					
Lys	Phe	Trp	Asn	Leu	Cys	Pro	Arg	Asp	Leu	Val	Pro	Lys	Gly	Ile						
				50					55					60						
ggt	aat	aag	gat	caa	caa	att	ggt	tat	tgg	aat	aga	cag	att	cgt	225					
Gly	Asn	Lys	Asp	Gln	Gln	Ile	Gly	Tyr	Trp	Asn	Arg	Gln	Ile	Arg						
				65					70					75						
tat	cgt	att	gta	aaa	ggc	cag	cgt	aag	gaa	ctc	gct	gag	agg	tgg	270					
Tyr	Arg	Ile	Val	Lys	Gly	Gln	Arg	Lys	Glu	Leu	Ala	Glu	Arg	Trp						
				80					85					90						
ttc	ttt	tac	ttc	tta	ggt	aca	gga	cct	cat	gct	gat	gct	aaa	ttc	315					
Phe	Phe	Tyr	Phe	Leu	Gly	Thr	Gly	Phe	His	Ala	Asp	Ala	Lys	Phe						
				95					100					105						
aaa	gac	aag	att	gat	gga	gtc	ttc	tgg	gtt	gca	agg	gat	ggt	gcc	360					
Lys	Asp	Lys	Ile	Asp	Gly	Val	Phe	Trp	Val	Ala	Arg	Asp	Gly	Ala						
				110					115					120						
atg	aac	aag	ccc	aca	acg	ctt	ggc	act	cgt	gga	acc	aat	aac	gaa	405					
Met	Asn	Lys	Pro	Thr	Thr	Leu	Gly	Thr	Arg	Gly	Thr	Asn	Asn	Glu						
				125					130					135						
tcc	aaa	cca	ctg	aga	ttt	gat	ggt	aag	ata	ccg	cca	cag	ttt	cag	450					
Ser	Lys	Pro	Leu	Arg	Phe	Asp	Gly	Lys	Ile	Pro	Pro	Gln	Phe	Gln						
				140					145					150						
ctt	gaa	gtg	aac	cgt	tct	agg	aac	aat	tca	agg	tct	ggt	tct	cag	495					
Leu	Glu	Val	Asn	Arg	Ser	Arg	Asn	Asn	Ser	Arg	Ser	Gly	Ser	Gln						
				155					160					165						
tct	aga	tct	gtt	tca	aga	aac	aga	tct	caa	tct	aga	gga	aga	cac	540					
Ser	Arg	Ser	Val	Ser	Arg	Asn	Arg	Ser	Gln	Ser	Arg	Gly	Arg	His						
				170					175					180						
cat	tcc	aat	aac	cag	aat	aat	aat	gtt	gag	gat	aca	att	gta	gcc	585					
His	Ser	Asn	Asn	Gln	Asn	Asn	Asn	Val	Glu	Asp	Thr	Ile	Val	Ala						
				185					190					195						

gtg	ctt	gaa	aaa	tta	ggt	ggt	act	gac	aaa	caa	agg	tca	cgt	tct	630
Val	Leu	Glu	Lys	Leu	Gly	Val	Thr	Asp	Lys	Gln	Arg	Ser	Arg	Ser	
				200					205					210	
aaa	cct	aga	gaa	cgt	agt	gat	tcc	aaa	cct	agg	gac	aca	aca	cct	675
Lys	Pro	Arg	Glu	Arg	Ser	Asp	Ser	Lys	Pro	Arg	Asp	Thr	Thr	Pro	
				215					220					225	
aag	aat	gcc	aac	aaa	cac	acc	tgg	aag	aaa	act	gca	ggc	aag	gga	720
Lys	Asn	Ala	Asn	Lys	His	Thr	Trp	Lys	Lys	Thr	Ala	Gly	Lys	Gly	
				230					235					240	
gat	gtg	aca	act	ttc	tat	ggt	gct	aga	agt	agt	tca	gct	aac	ttt	765
Asp	Val	Thr	Thr	Phe	Tyr	Gly	Ala	Arg	Ser	Ser	Ser	Ala	Asn	Phe	
				245					250					255	
ggt	gat	agt	gat	ctc	gtt	gcc	aat	ggt	aac	gct	gcc	aaa	tgc	tac	810
Gly	Asp	Ser	Asp	Leu	Val	Ala	Asn	Gly	Asn	Ala	Ala	Lys	Cys	Tyr	
				260					265					270	
cct	cag	ata	gct	gaa	tgt	gtt	cca	tca	gtg	tct	agc	ata	atc	ttt	855
Pro	Gln	Ile	Ala	Glu	Cys	Val	Pro	Ser	Val	Ser	Ser	Ile	Ile	Phe	
				275					280					285	
ggc	agt	caa	tgg	tct	gct	gaa	gaa	gct	ggt	gat	caa	gtg	aaa	gtc	900
Gly	Ser	Gln	Trp	Ser	Ala	Glu	Glu	Ala	Gly	Asp	Gln	Val	Lys	Val	
				290					295					300	
acg	ctc	act	cac	acc	tac	tac	ctg	cca	aag	gat	gat	gcc	aaa	act	945
Thr	Leu	Thr	His	Thr	Tyr	Tyr	Leu	Pro	Lys	Asp	Asp	Ala	Lys	Thr	
				305					310					315	
agt	caa	ttc	cta	gaa	cag	att	gac	gct	tac	aag	cga	cct	tct	gaa	990
Ser	Gln	Phe	Leu	Glu	Gln	Ile	Asp	Ala	Tyr	Lys	Atg	Pro	Ser	Glu	
				320					325					330	
gtg	gct	aag	gat	cag	agg	caa	aga	aga	tcc	cgt	tct	aag	tct	gct	1035
Val	Ala	Lys	Asp	Gln	Arg	Gln	Arg	Arg	Ser	Arg	Ser	Lys	Ser	Ala	
				335					340					345	
gat	aag	aag	cct	gag	gag	ttg	tct	gta	act	ctt	gtg	gag	gca	tac	1080
Asp	Lys	Lys	Pro	Glu	Glu	Lys	Ser	Val	Thr	Leu	Val	Glu	Ala	Tyr	
				350					355					360	
aca	gat	gtg	ttt	gat	gac	aca	cag	gtt	gag	atg	att	gat	gag	gtt	1125

Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val
 365 370 375

acg aac taa acgcatgctc 1144

Thr Asn

377

<210> 19

<211> 1979

<212> DNA

<213> feline leukemia virus

<220>

<223>

<400> 1

accaccaatc aagacctctc ggacagcccc agctcjjigacg atccatcaag 50

atg gaa agt cca acg cac cca aaa ccc tct aaa gat aag act ctc 95

Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu

1

5

10

15

tgc tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac 140

Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp

20

25

30

ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act 185

Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr

35

40

45

tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc 230

Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr

50

55

60

tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt 275

Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val

65

70

75

gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta 320

Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu

09073831.060404

	80	85	90	
aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa	365			
Asn Pro Thr Asn'Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys				
	95	100	105	
tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac	410			
Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr				
	110	115	120	
ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag	455			
Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys				
	125	130	135	
gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg	500			
Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp				
	140	145	150	
gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca	545			
Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser				
	155	160	165	
tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc	590			
Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser				
	170	175	180	
tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag	635			
Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys				
	185	190	195	
gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga	680			
Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg				
	200	205	210	
cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc	725			
Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser				
	215	220	225	
cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac	770			
Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn				
	230	235	240	
cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca	815			
Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr				

				245					250					255	
ggg	tcc	aaa	gtg	gcg	acc	cag	agg	ccc	caa	acg	aat	gaa	agc	gcc	860
Gly	Ser	Lys	Val	Ala	Thr	Gln	Arg	Pro	Gln	Thr	Asn	Glu	Ser	Ala	
				260					265					270	
cca	agg	tct	gtt	gcc	ccc	acc	acc	atg	ggt	ccc	aaa	cgg	att	ggg	905
Pro	Arg	Ser	Val	Ala	Pro	Thr	Thr	Met	Gly	Pro	Lys	Arg	Ile	Gly	
				275					280					285	
acc	gga	gat	agg	tta	ata	aat	tta	gta	caa	ggg	aca	tac	cta	gcc	950
Thr	Gly	Asp	Arg	Leu	Ile	Asn	Leu	Val	Gln	Gly	Thr	Tyr	Leu	Ala	
				290					295					300	
tta	aat	gcc	acc	gac	ccc	aac	aaa	act	aaa	gac	tgt	tgg	ctc	tgc	995
Leu	Asn	Ala	Thr	Asp	Pro	Asn	Lys	Thr	Lys	Asp	Cys	Trp	Leu	Cys	
				305					310					315	
ctg	gtt	tct	cga	cca	ccc	tat	tac	gaa	ggg	att	gca	atc	tta	ggt	1040
Leu	Val	Ser	Arg	Pro	Pro	Tyr	Tyr	Glu	Gly	Ile	Ala	Ile	Leu	Gly	
				320					325					330	
acc	tac	agc	aac	caa	aca	aac	ccc	ccc	cca	tcc	tgc	cta	tct	act	1085
Asn	Tyr	Ser	Asn	Gln	Thr	Asn	Pro	Pro	Pro	Ser	Cys	Leu	Ser	Ile	
				335					340					345	
ccg	caa	cac	aaa	cta	act	ata	tct	gaa	gta	tca	ggg	caa	gga	atg	1130
Pro	Gln	His	Lys	Leu	Thr	Ile	Ser	Glu	Val	Ser	Gly	Gln	Gly	Met	
				350					355					360	
tgc	ata	ggg	act	gtt	cct	aaa	acc	cac	cag	gct	ttg	tgc	aat	aag	1175
Cys	Ile	Gly	Thr	Val	Pro	Lys	Thr	His	Gln	Ala	Leu	Cys	Asn	Lys	
				365					370					375	
aca	caa	cag	gga	cat	aca	ggg	gcg	cac	tat	cta	gcc	gcc	ccc	aac	1220
Thr	Gln	Gln	Gly	His	Thr	Gly	Ala	His	Tyr	Leu	Ala	Ala	Pro	Asn	
				380					385					390	
ggc	acc	tat	tgg	gcc	tgt	aac	act	gga	ctc	acc	cca	tgc	att	tcc	1265
Gly	Thr	Tyr	Trp	Ala	Cys	Asn	Thr	Gly	Leu	Thr	Pro	Cys	Ile	Ser	
				395					400					405	

atg	gcg	gtg	ctc	aat	tgg	acc	tct	gat	ttt	tgt	gtc	tta	atc	gaa	1310
Met	Ala	Val	Leu	Asn	Trp	Thr	Ser	Asp	Phe	Cys	Val	Leu	Ile	Glu	
				410					415					420	
tta	tgg	ccc	aga	gtg	act	tac	cat	caa	ccc	gaa	tat	gtg	tac	aca	1355
Leu	Trp	Pro	Arg	Val	Thr	Tyr	His	Gln	Pro	Glu	Tyr	Val	Tyr	Thr	
				425					430					435	
cat	ttt	gcc	aaa	gct	gtc	agg	ttc	cga	aga	gaa	cca	ata	tca	cta	1400
His	Phe	Ala	Lys	Ala	Val	Arg	Phe	Arg	Axg	Glu	Pro	Ile	Ser	Leu	
				440					445					450	
acg	gtt	gcc	ctt	atg	ttg	gga	gga	ctt	act	gta	ggg	ggc	ata	gcc	1445
Thr	Val	Ala	Leu	Met	Leu	Gly	Gly	Leu	Thr	Val	Gly	Gly	Ile	Ala	
				455					460					465	
gcg	ggg	gtc	gga	aca	ggg	act	aaa	gcc	ctc	ctt	gaa	aca	gcc	cag	1490
Ala	Gly	Val	Gly	Thr	Gly	Thr	Lys	Ala	Leu	Leu	Glu	Thr	Ala	Gln	
				470					475					480	
ttc	aga	caa	cta	caa	atg	gcc	atg	cac	aca	gac	atc	cag	gcc	cta	1535
Phe	Arg	Gln	Leu	Gln	Met	Ala	Met	His	Thr	Asp	Ile	Gln	Ala	Leu	
				485					490					495	
gaa	gaa	tca	att	agt	gcc	tta	gaa	aag	tcc	ctg	acc	tcc	ctt	tct	1580
Glu	Glu	Ser	Ile	Ser	Ala	Leu	Glu	Lys	Ser	Leu	Thr	Ser	Leu	Ser	
				500					505					510	
gaa	gta	gtc	tta	caa	aac	aga	cgg	ggc	cta	gat	att	cta	ttc	tta	1625
Glu	Val	Val	Leu	Gln	Asn	Arg	Arg	Glu	Leu	Asp	Ile	Leu	Phe	Leu	
				515					520					525	
caa	gag	gga	ggg	ctc	tgt	gcc	gca	ttg	aaa	gaa	gaa	tgt	tgc	ttc	1670
Gln	Glu	Gly	Gly	Leu	Cys	Ala	Ala	Leu	Lys	Glu	Glu	Cys	Cys	Phe	
				530					535					540	
tat	gcg	gat	cac	acc	gga	ctc	gtc	cga	gac	aat	atg	gcc	aaa	tta	1715
Tyr	Ala	Asp	His	Thr	Gly	Leu	Val	Arg	Asp	Asn	Met	Ala	Lys	Leu	
				545					550					555	
aga	gaa	aga	cta	aaa	cag	cgg	caa	caa	ctg	ttt	gac	tcc	caa	cag	1760
Arg	Glu	Arg	Leu	Lys	Gln	Arg	Gln	Gln	Leu	Phe	Asp	Ser	Gln	Gln	
				560					565					570	

gga tgg ttt gaa gga tgg ttc aac aag tcc ccc tgg ttt aca acc 1805
 Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp Phe Thr Thr
 575 580 585

cta att tcc tcc att atg ggc ccc tta cta atc cta ctc cta att 1850
 Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Leu Ile
 590 595 600

ctc ctc ttc ggc cca tgc atc ctt aac cga tta gta caa ttc gta
 1895 Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe
 Val
 605 610 615

aaa gac aga ata tct gtg gta cag gct tta att tta acc caa cag
 1940 Lys Asp Axg Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln
 Gln
 620 625 630

tac caa cag ata aag caa tac gat ccg gac cga cca tga 1979
 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro
 635 640

<210> 20

<211> 584

<212> PRT

<213> feline panleukopenia peritonitis virus

<220>

<223>

<400> 1

Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val
 5 10 15

Arg Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly
 20 25 30

Gly Gly Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe
 35 40 45

09073331 060401

Asn	Asn	Gln	Thr	Glu	Phe	Lys	Phe	Leu	Glu	Asn	Gly	Trp	Val	Glu	
				50					55					60	
Ile	Thr	Ala	Asn	Ser	Ser	Arg	Leu	Val	His	Leu	Asn	Met	Pro	Glu	
				65					70					75	
Ser	Glu	Asn	Tyr	Lys	Arg	Val	Val	Val	Asn	Asn	Met	Asp	Lys	Thr	
				80					85					90	
Ala	Val	Lys	Gly	Asn	Met	Ala	Leu	Asp	Asp	Thr	His	Val	Gln	Ile	
				95					100					105	
Val	Thr	Pro	Trp	Ser	Leu	Val	Asp	Ala	Asn	Ala	Trp	Gly	Val	Trp	
				110					115					120	
Phe	Asn	Pro	Gly	Asp	Trp	Gln	Leu	Ile	Val	Asn	Thr	Met	Ser	Glu	
				125					130					135	
Leu	His	Leu	Val	Ser	Phe	Glu	Gln	Glu	Ile	Phe	Asn	Val	Val	Leu	
				140					145					150	
Lys	Thr	Val	Ser	Glu	Ser	Ala	Thr	Gln	Pro	Pro	Thr	Lys	Val	Tyr	
				155					160					165	
Asn	Asn	Asp	Leu	Thr	Ala	Ser	Leu	Met	Val	Ala	Leu	Asp	Ser	Asn	
				170					175					180	
Asn	Thr	Met	Pro	Phe	Thr	Pro	Ala	Ala	Met	Arg	Ser	Glu	Thr	Leu	
				185					190					195	
Gly	Phe	Tyr	Pro	Trp	Lys	Pro	Thr	Ile	Pro	Thr	Pro	Trp	Arg	Tyr	
				200					205					210	
Tyr	Phe	Gln	Trp	Asp	Arg	Thr	Leu	Ile	Pro	Ser	His	Thr	Gly	Thr	
				215					220					225	
Ser	Gly	Thr	Pro	Thr	Asn	Ile	Tyr	His	Gly	Thr	Asp	Pro	Asp	Asp	
				230					235					240	
Val	Gln	Phe	Tyr	Thr	Ile	Glu	Asn	Ser	Val	Pro	Val	His	Leu	Leu	
				245					250					255	
Arg	Thr	Gly	Asp	Glu	Phe	Ala	Thr	Gly	Thr	Phe	Phe	Phe	Asp	Cys	
				260					265					270	

Lys Pro Cys Arg Leu Thr His Thr Trp Gln Thr Asn Axg Ala Leu
275 280 285

Gly Leu Pro Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala
290 295 300

Thr Asn Phe Gly Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly
305 310 315

Val Thr Gln Met Gly Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile
320 325 330

Met Arg Pro Ala Glu Val Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe
335 340 345

Glu Ala Ser Thr Gln Gly Pro Phe Lys Ile Pro Ile Ala Ala Gly
350 355 360

Arg Gly Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala Asp Gly Asp
365 370 375

Pro Arg Tyr Ala Phe Gly Arg Gln His Gly Gln Lys Thr Thr Thr
380 385 390

Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr Ile Ala His Gln Asp
395 400 405

Thr Gly Arg Tyr Pro Ala Gly Asp Trp Ile Gln Asn Ile Asn Phe
410 415 420

Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro Thr Asp Pro
425 430 435

Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn Thr
440 445 450

Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro
455 460 465

Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro
470 475 480

Cys Pro Asn Asn Leu Val Val Glu Asp Glu Gly Cys Thr Asn
45 50 55

Leu Ser Gly Phe Ser Tyr Met Glu Leu Lys Val Gly Tyr Ile
60 65 70

Leu Ala Ile Lys Met Asn Gly Phe Thr Cys Thr Gly Val Val
75 80

Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr Val Thr
85 90 95

Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
100 105 110

Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg
115 120 125

Tyr Glu Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp
130 135 140

Leu Arg Thr Val Lys Thr Thr Lys Glu Ser Leu Val Ile Ile
145 150

Ser Pro Ser Val Ala Asp Leu Asp Pro Tyr Asp Arg Ser Leu
155 160 165

His Ser Arg Val Phe Pro Ser Gly Lys Cys Ser Gly Val Ala
170 175 180

Val Ser Ser Thr Tyr Cys Ser Thr Asn His Asp Tyr Thr Ile
185 190 195

Trp Met Pro Glu Asn Pro Arg Leu Gly Met Ser Cys Asp Ile
200 205 210

Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Lys Gly Ser Glu
215 220

Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu
225 230 235

Lys Gly Ala Cys Lys Leu Lys Leu Cys Gly Val Leu Gly Leu
240 245 250

Arg	Leu	Met	Asp	Gly	Thr	Trp	Val	Ala	Met	Gln	Thr	Ser	Asn	
255						260			265					
Glu	Thr	Lys	Trp	Cys	Pro	Pro	Asp	Gln	Leu	Val	Asn	Leu	His	
			270						275					
280														
Asp	Phe	Arg	Ser	Asp	Glu	Ile	Glu	His	Leu	Val	Val	Glu	Glu	
				285						290				
Leu	Val	Arg	Lys	Arg	Glu	Glu	Cys	Leu	Asp	Ala	Leu	Glu	Ser	
295					300						305			
Ile	Met	Thr	Thr	Lys	Ser	Val	Ser	Phe	Arg	Arg	Leu	Ser	His	
310					315						320			
Leu	Arg	Lys	Leu	Val	Pro	Gly	Phe	Gly	Lys	Ala	Tyr	Thr	Ile	
		325					330							335
Phe	Asn	Lys	Thr	Leu	Met	Glu	Ala	Asp	Ala	His	Tyr	Lys	Ser	
			340					345						350
Val	Arg	Thr	Trp	Asn	Glu	Ile	Leu	Pro	Ser	Lys	Gly	Cys	Leu	
				355					360					
Arg	Val	Gly	Gly	Arg	Cys	His	Pro	His	Val	Asn	Gly	Val	Phe	
365					370					375				
Phe	Asn	Gly	Ile	Ile	Leu	Gly	Pro	Asp	Gly	Asn	Val	Leu	Ile	
380					385						390			
Pro	Glu	Met	Gln	Ser	Ser	Leu	Leu	Gln	Gln	His	Met	Glu	Leu	
			395		400						405			
Leu	Glu	Ser	Ser	Val	Ile	Pro	Leu	Val	His	Pro	Leu	Ala	Asp	
			410					415						420
Pro	Ser	Thr	Val	Phe	Lys	Asp	Gly	Asp	Glu	Ala	Glu	Asp	Phe	
				425					430					
Val	Glu	Val	His	Leu	Pro	Asp	Val	His	Asn	Gln	Val	Ser	Gly	
435					440					445				
Val	Asp	Leu	Gly	Leu	Pro	Asn	Trp	Gly	Lys	Tyr	Val	Leu	Leu	
450					455						460			

Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu
 465 470 475

Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln
 480 485 490

His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro
 495 500

Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser
 505 510 515

Gly Gly Glu Thr Arg Leu
 520 524

<210> 22

<211> 668

<212> PRT

<213> feline calicivirus

<220>

<223>

<400> 1

Met Cys Ser Thr Cys Ala Asn Val Leu Lys Tyr Tyr Asp Trp Asp
 1 5 10 15

Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val
 20 25 30

Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu
 35 40 45

Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln
 50 55 60

Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr
 65 70 75

His	Glu	Ala	Ile	Asp	Pro	Val	Val	Pro	Pro	Met	His	Trp	Asp	Glu	80	85	90
Ala	Gly	Lys	Ile	Phe	Gln	Pro	His	Pro	Gly	Val	Leu	Met	His	His	95	100	105
Leu	Ile	Cys	Lys	Val	Ala	Glu	Gly	Trp	Asp	Pro	Asn	Leu	Pro	Leu	110	115	120
Phe	Arg	Leu	Glu	Ala	Asp	Asp	Gly	Ser	Ile	Thr	Thr	Pro	Glu	Gln	125	130	135
Gly	Thr	Met	Val	Gly	Gly	Val	Ile	Ala	Glu	Pro	Asn	Ala	Gln	Met	140	145	150
Ser	Thr	Ala	Ala	Asp	Met	Ala	Thr	Gly	Lys	Ser	Val	Asp	Ser	Glu	155	160	165
Trp	Glu	Ala	Phe	Phe	Ser	Phe	His	Thr	Ser	Val	Asn	Trp	Ser	Thr	170	175	180
Ser	Glu	Thr	Gln	Gly	Lys	Ile	Leu	Phe	Lys	Gln	Ser	Leu	Gly	Pro	185	190	195
Leu	Leu	Asn	Pro	Tyr	Leu	Thr	His	Leu	Ala	Lys	Leu	Tyr	Val	Ala	200	205	210
Trp	Ser	Gly	Ser	Val	Asp	Val	Arg	Phe	Ser	Ile	Ser	Gly	Ser	Gly	215	220	225
Val	Phe	Gly	Gly	Lys	Leu	Ala	Ala	Ile	Val	Val	Pro	Pro	Gly	Ile	230	235	240
Asp	Pro	Val	Gln	Ser	Thr	Ser	Met	Leu	Gln	Tyr	Pro	His	Val	Leu	245	250	255
Phe	Asp	Ala	Arg	Gln	Val	Glu	Pro	Val	Ile	Phe	Ser	Ile	Pro	Asp	260	265	270
Leu	Arg	Ser	Thr	Leu	Tyr	His	Leu	Met	Ser	Asp	Thr	Asp	Thr	Thr	275	280	285
Ser	Leu	Val	Ile	Met	Val	Tyr	Asn	Asp	Leu	Ile	Asn	Pro	Tyr	Ala	290	295	300

Asn	Asp	Ser	Asn	Ser	Ser	Gly	Cys	Ile	Val	Thr	Val	Glu	Thr	Lys	305	310	315
Pro	Gly	Pro	Asp	Phe	Lys	Phe	His	Leu	Leu	Lys	Pro	Pro	Gly	Ser	320	325	330
Met	Leu	Thr	His	Gly	Ser	Ile	Pro	Ser	Asp	Leu	Ile	Pro	Lys	Ser	335	340	345
Ser	Ser	Leu	Trp	Ile	Gly	Asn	Arg	Phe	Trp	Ser	Asp	Ile	Thr	Asp	350	355	360
Phe	Val	Ile	Arg	Pro	Phe	Val	Phe	Gln	Ala	Asn	Arg	His	Phe	Asp	365	370	375
Phe	Asn	Gln	Glu	Thr	Ala	Gly	Trp	Ser	Thr	Pro	Arg	Phe	Arg	Pro	380	385	390
Ile	Thr	Ile	Thr	Ile	Ser	Val	Lys	Glu	Ser	Ala	Lys	Leu	Gly	Ile	395	400	405
Gly	Val	Ala	Thr	Asp	Tyr	Ile	Val	Pro	Gly	Ile	Pro	Asp	Gly	Trp	410	415	420
Pro	Asp	Thr	Thr	Ile	Pro	Gly	Glu	Leu	Val	Pro	Val	Gly	Asp	Tyr	425	430	435
Ala	Ile	Thr	Asn	Gly	Thr	Asn	Asn	Asp	Ile	Thr	Thr	Ala	Ala	Gln	440	445	450
Tyr	Asp	Ala	Ala	Thr	Glu	Ile	Arg	Asn	Asn	Thr	Asn	Phe	Arg	Gly	455	460	465
Met	Tyr	Ile	Cys	Gly	Ser	Leu	Gln	Arg	Ala	Trp	Gly	Asp	Lys	Lys	470	475	480
Ile	Ser	Asn	Thr	Ala	Phe	Ile	Thr	Thr	Gly	Thr	Val	Asp	Gly	Ala	485	490	495
Lys	Leu	Ile	Pro	Ser	Asn	Thr	Ile	Asp	Gln	Thr	Lys	Ile	Ala	Val	500	505	510
Phe	Gln	Asp	Thr	His	Ala	Asn	Lys	His	Val	Gln	Thr	Ser	Asp	Asp	515	520	525

1	5	10	15
Tyr Gly Glu Arg	Tyr Cys Ala Met	Gln Asp Ser Gly	Leu Gln Cys
	20	25	30
Ile Gln Gly Thr	Gln Ser Arg Cys	Gln Thr Cys Phe	Glu Arg Gly
	35	40	45
Asp Leu Ile Trp	His Leu Ala Asn	Trp Asn Phe Ser	Trp Ser Val
	50	55	60
Ile Leu Ile Val	Phe Ile Thr Val	Leu Gln Tyr Gly	Arg Pro Gln
	65	70	75
Phe Ser Trp Leu	Val Tyr Gly Ile	Lys Met Leu Ile	Met Trp Leu
	80	85	90
Leu Trp Pro Ile	Val Leu Ala Leu	Thr Ile Phe Asn	Ala Tyr Ser
	95	100	105
Glu Tyr Gln Val	Ser Arg Tyr Val	Met Phe Gly Phe	Ser Val Ala
	110	115	120
Gly Ala Val Val	Thr Phe Ala Leu	Trp Met Met Tyr	Phe Val Arg
	125	130	135
Ser Val Gln Leu	Tyr Arg Axx Thr	Lys Ser Trp Trp	Ser Phe Asn
	140	145	150
Pro Glu Thr Asn	Ala Ile Leu Cys	Val Asn Ala Leu	Gly Arg Ser
	155	160	165
Tyr Val Leu Pro	Leu Asp Gly Thr	Pro Thr Gly Val	Thr Leu Thr
	170	175	180
Leu Leu Ser Gly	Asn Leu Tyr Ala	Glu Gly Phe Lys	Met Ala Gly
	185	190	195
Gly Leu Thr Ile	Glu His Leu Pro	Lys Tyr Val Met	Ile Ala Thr
	200	205	210
Pro Ser Arg Thr	Ile Val Tyr Thr	Ile Val Gly Lys	Gln Leu Lys
	215	220	225
Ala Thr Thr Ala	Thr Gly Trp Ala	Tyr Tyr Val Lys	Ser Lys Ala

09073001.0040401
"04090" T88E4860

	230		235		240
Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His					
	245		250		255
Glu Lys Leu Leu His Met Val					
	260				

<210> 24

<211> 377

<212> PRT

<213> feline infectious peritonitis virus

<220>

<223>

<400> 1

Met	Ala	Thr	Gln	Gly	Gln	Arg	Val	Asn	Trp	Gly	Asp	Glu	Pro	Ser
1				5					10					15

Lys	Arg	Arg	Gly	Arg	Ser	Asn	Ser	Arg	Gly	Arg	Lys	Asn	Asn	Asp
				20					25					30

Ile	Pro	Leu	Ser	Phe	Tyr	Asn	Phe	Ile	Thr	Leu	Glu	Gln	Glu	Ser
				35					40					45

Lys	Phe	Trp	Asn	Leu	Cys	Pro	Arg	Asp	Leu	Val	Pro	Lys	Gly	Ile
				50					55					60

Gly	Asn	Lys	Asp	Gln	Gln	Ile	Gly	Tyr	Trp	Asn	Arg	Gln	Ile	Arg
				65					70					75

Tyr	Arg	Ile	Val	Lys	Gly	Gln	Arg	Lys	Glu	Leu	Ala	Glu	Arg	Trp
				80					85					90

Phe Phe Tyr Phe Leu Gly Thr Gly Phe His Ala Asp Ala Lys Phe
95 100 105

Lys Asp Lys Ile Asp Gly Val Phe Trp Val Ala Arg Asp Gly Ala
110 115 120

Met Asn Lys Pro Thr Thr Leu Gly Thr Arg Gly Thr Asn Asn Glu
125 130 135

Ser Lys Pro Leu Arg Phe Asp Gly Lys Ile Pro Pro Gln Phe Gln
140 145 150

Leu Glu Val Asn Arg Ser Arg Asn Asn Ser Arg Ser Gly Ser Gln
155 160 165

Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser Arg Gly Arg His
170 175 180

His Ser Asn Asn Gln Asn Asn Asn Val Glu Asp Thr Ile Val Ala
185 190 195

Val Leu Glu Lys Leu Gly Val Thr Asp Lys Gln Arg Ser Arg Ser
200 205 210

Lys Pro Arg Glu Arg Ser Asp Ser Lys Pro Arg Asp Thr Thr Pro
215 220 225

Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly
230 235 240

Asp Val Thr Thr Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe
245 250 255

<223>

<400> 1

Met	Glu	Ser	Pro	Thr	His	Pro	Lys	Pro	Ser	Lys	Asp	Lys	Thr	Leu	
1				5					10					15	
Ser	Trp	Asn	Leu	Ala	Phe	Leu	Val	Gly	Ile	Leu	Phe	Thr	Ile	Asp	
				20					25					30	
Ile	Gly	Met	Ala	Asn	Pro	Ser	Pro	His	Gln	Ile	Tyr	Asn	Val	Thr	
				35					40					45	
Trp	Val	Ile	Thr	Asn	Val	Gln	Thr	Asn	Thr	Gln	Ala	Asn	Ala	Thr	
				50					55					60	
Ser	Met	Leu	Gly	Thr	Leu	Thr	Asp	Ala	Tyr	Pro	Thr	Leu	His	Val	
				65					70					75	
Asp	Leu	Cys	Asp	Leu	Val	Gly	Asp	Thr	Trp	Glu	Pro	Ile	Val	Leu	
				80					85					90	
Asn	Pro	Thr	Asn	Val	Lys	His	Gly	Ala	Arg	Tyr	Ser	Ser	Ser	Lys	
				95					100					105	
Tyr	Gly	Cys	Lys	Thr	Thr	Asp	Arg	Lys	Lys	Gln	Gln	Gln	Thr	Tyr	
				110					115					120	
Pro	Phe	Tyr	Val	Cys	Pro	Gly	His	Ala	Pro	Ser	Leu	Gly	Pro	Lys	
				125					130					135	
Gly	Thr	His	Cys	Gly	Gly	Ala	Gln	Asp	Gly	Phe	Cys	Ala	Ala	Trp	
				140					145					150	
Gly	Cys	Glu	Thr	Thr	Gly	Glu	Thr	Trp	Trp	Lys	Pro	Thr	Ser	Ser	
				155					160					165	
Trp	Asp	Tyr	Ile	Thr	Val	Lys	Arg	Gly	Ser	Ser	Gln	Asp	Asn	Ser	
				170					175					180	
Cys	Glu	Gly	Lys	Cys	Asn	Pro	Leu	Val	Leu	Gln	Phe	Thr	Gln	Lys	
				185					190					195	
Gly	Arg	Gln	Ala	Ser	Trp	Asp	Gly	Pro	Lys	Met	Trp	Gly	Leu	Arg	
				200					205					210	

Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser	215	220	225
Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn	230	235	240
Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr	245	250	255
Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala	260	265	270
Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly	275	280	285
Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala	290	295	300
Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys	305	310	315
Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly	320	325	330
Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile	335	340	345
Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met	350	355	360
Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys	365	370	375
Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn	380	385	390
Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser	395	400	405
Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu	410	415	420
Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr	425	430	435

09873260
T04090" T88E.2650

His	Phe	Ala	Lys	Ala	Val	Arg	Phe	Arg	Axg	Glu	Pro	Ile	Ser	Leu	440	445	450
Thr	Val	Ala	Leu	Met	Leu	Gly	Gly	Leu	Thr	Val	Gly	Gly	Ile	Ala	455	460	465
Ala	Gly	Val	Gly	Thr	Gly	Thr	Lys	Ala	Leu	Leu	Glu	Thr	Ala	Gln	470	475	480
Phe	Arg	Gln	Leu	Gln	Met	Ala	Met	His	Thr	Asp	Ile	Gln	Ala	Leu	485	490	495
Glu	Glu	Ser	Ile	Ser	Ala	Leu	Glu	Lys	Ser	Leu	Thr	Ser	Leu	Ser	500	505	510
Glu	Val	Val	Leu	Gln	Asn	Arg	Arg	Glu	Leu	Asp	Ile	Leu	Phe	Leu	515	520	525
Gln	Glu	Gly	Gly	Leu	Cys	Ala	Ala	Leu	Lys	Glu	Glu	Cys	Cys	Phe	530	535	540
Tyr	Ala	Asp	His	Thr	Gly	Leu	Val	Arg	Asp	Asn	Met	Ala	Lys	Leu	545	550	555
Arg	Glu	Arg	Leu	Lys	Gln	Arg	Gln	Gln	Leu	Phe	Asp	Ser	Gln	Gln	560	565	570
Gly	Trp	Phe	Glu	Gly	Trp	Phe	Asn	Lys	Ser	Pro	Trp	Phe	Thr	Thr	575	580	585
Leu	Ile	Ser	Ser	Ile	Met	Gly	Pro	Leu	Leu	Ile	Leu	Leu	Leu	Ile	590	595	600
Leu	Leu	Phe	Gly	Pro	Cys	Ile	Leu	Asn	Arg	Leu	Val	Gln	Phe	Val	605	610	615
Lys	Asp	Axg	Ile	Ser	Val	Val	Gln	Ala	Leu	Ile	Leu	Thr	Gln	Gln	620	625	630
Tyr	Gln	Gln	Ile	Lys	Gln	Tyr	Asp	Pro	Asp	Arg	Pro				635	640	